

Report for 2005ND76B: Molecular Phylogeography of *Etheostoma Nigrum* in the Northern Midwest

Publications

- There are no reported publications resulting from this project.

Report Follows

MOLECULAR PHYLOGEOGRAPHY OF *ETHEOSTOMA NIGRUM* (RAFINESQUE) IN THE UPPER MIDWEST

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WATER PROBLEM AND OBJECTIVES

The geologic history and abundant potential study sites of the upper Midwest provide a unique opportunity for the assessment of spatial genetic diversity. The Johnny Darter, *Etheostoma nigrum* (Rafinesque), with its large range and abundant populations, is an excellent species to study to answer phylogeographic questions about North Dakota and Minnesota. In this study, the genetic diversity of *E. nigrum* will be examined by using microsatellite PCR primers designed initially for other species of *Etheostoma* and recently optimized for *E. nigrum*. This information will provide not only the inferred gene flow among the darters but will also provide a baseline against which to evaluate gene flow for other fish species located in the same water bodies. For instance, many game fish are stocked and transferred within and among watersheds with no genetic monitoring. By studying a benthic fish with a small home range, it will be possible to uncover the phylogeographic structure among the various watersheds of the upper Midwest. In turn, this information can be used by managers for conserving genetic diversity within and among watersheds.

This project uses molecular markers and their application in conservation ecology and as such the project spans the fields of ecology and genetics. More specifically, microsatellite markers will be used to examine the genetic relationships among *Etheostoma nigrum* (Johnny Darter) populations in the northern Midwest, specifically North Dakota and Minnesota.



Seining a Minnesota Stream Spring 2005



E. nigrum taken from Lake Ida, MN, Spring 2005



**Sampling site on Upper Mississippi River
Minnesota, Summer 2005**



**Sampling Site on Fish Hook River
Minnesota, Summer 2005**

PROJECT PROGRESS

During the spring, summer and fall of 2005, 408 individuals were captured from the Upper Missouri River, Red River of the North, and Upper Mississippi River watersheds. DNA was extracted from fin clips taken from each fish. This DNA is currently being used to optimize microsatellite makers to examine genetic diversity within and among the

sampled populations. To evaluate genetic structure, we are examining 9 microsatellite loci using primers developed for congeners of *E. nigrum*. We have been able to consistently amplify eight microsatellites, but one requires further optimization for use with *E. nigrum*. Of the 4 loci most thoroughly examined, heterozygosities ranged from 0.0% to 84.7% with allelic richness between 1 and 28. Within the richest locus, individual populations (k=5, n=59) appear to differ in genetic structure and distribution of alleles.

SIGNIFICANCE OF RESEARCH

The genetic evaluation of *E. nigrum* populations may have management implications. Most of the fish populations in the upper Midwest have been isolated since the end of the Pleistocene. Managers often transfer and stock game fish from one water body to another with little to no regard for the genetic structure of the systems. This practice is occasionally based upon the idea that gene flow will occur in systems that are hydrologically connected; but in actuality, gene flow is largely influenced by the migratory habits of individual species. Species with small home ranges may have little gene flow between closely located populations. Over time, these populations develop a unique genetic identity, often adapting to local conditions. When fish transfers are planned without consideration of this diversity, populations become genetically homogenous. This results in a loss of genetic variation among populations and perhaps even outbreeding depression. This is especially important if populations are locally adapted. Understanding the current diversity and gene flow of *E. nigrum* in the watersheds of the upper Midwest will aid in the establishment of management and conservation units as well as help managers plan for the transfer and stocking of fishes. *E. nigrum* are particularly useful for evaluating phylogeographic structure because they are non-migratory and unlikely to be accidentally transferred due to their use of benthic habitats. The optimization of published primers for use on *E. nigrum* will provide an excellent opportunity for not only this study but for future molecular work on Johnny Darters throughout their range. This project will provide a baseline with which other species and populations may be compared. Once the genetic relationships among this species are better understood and the diversity is used to help managers and scientists in this area, the information could potentially be used to manage congeners throughout the range of *Etheostoma nigrum*.